/30 **JC20 Rec'd PCT/PTO** 2 3 JUN 2005

SEQUENCE LISTING

<110> Takeda Pharmaceutical Company Limited
<120> Novel protein and its use
<130> 3132WOOP
<150> JP2002-378052
<151> 2002-12-26
<150> JP2003-65497
<151> 2003-03-11
<160> 25
<210> 1
<211> 837
<212> PRT
<213> Human
<400≻ 1
Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro Trp
5 10 15
Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu Leu
20 25 30
Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser Pro Arg Ile
35 40 45
Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu Arg Phe Glu Ala
50 55 60
Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu Ser Arg Asp Gly Arg
65 70 75 80
Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Leu Ser Ser Asn
85 90 95
Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala
100 105 110
Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys Gly Lys Asp Pro Gln

		115					120					125			
Arg	Asp	Cys	Gln	Asn	Tyr	Ile	Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser
	130					135					140				
His	Leu	Phe	Thr	Cys	Gly	Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr
145					150					155					160
Ile	Asn	Met	Glu	Asn	Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val
				165					170					175	
Leu	Leu	Glu	Asp	G1y	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys
			180					185					190		
Ser	Thr	Ala	Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser
		195					200					205			
Ser	Phe	Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg
,	210					215					220				
Pro	Thr	Lys	Ťhr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe
225					230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	G1y	Asp
				245					250					255	
Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe		Glu	Thr	Gly	Gln		Phe	Glu
			260					265					270	_	
Phe	Phe		Asn	Thr	Ile	Val		Arg	Ile	Ala	Arg		Cys	Lys	Gly
		275					280	0.1	0.1		<i>m</i>	285	0	DI	,
Asp		Gly	Gly	Glu	Arg		Leu	GIn	Gln	Arg		Thr	Ser	Phe	Leu
•	290	0.1		,	•	295		n.	A	A	300	Dl	D	DL -	۸
	Ala	Gin	Leu	Leu		ser	Arg	Pro	Asp		GIY	rne	rro	rne	320
305	1	C1-	1 an	Vol	310	Thm	Lou	Son	Dro	315	Dro	Gln	Acn	Trn	
vai	Leu	GIII	ASP	325		1111	Leu	Set	Pro 330	361	110	GIII	лър	335	nig
Acn	Thr	Lou	Pho			Val	Pho	Thr	Ser	Gln	Trn	His	Aro		Thr
лор	1111	Leu	340	1 91	Oly	741	1110	345	501	0111	11 p	1110	350	01)	
Thr	Glu	Glv		Ala	Val	Cvs	Val		Thr	Met	Lvs	Asp		Gln	Arg
****	014	355	501			0,0	360				-, -	365			
Val	Phe		Glv	Leu	Tvr	Lvs		Val	Asn	Arg	Glu		Gln	Gln	Met
	370				•	375				Ū	380				
Val		Arg	Asp	Pro	Pro		Pro	Thr	Pro	Arg			Ala	Cys	Ile
385		J	•		390					395					400
	Asn	Ser	Ala	Arg		Arg	Lys	Ile	Asn			Leu	Gln	Leu	Pro
				405					410					415	

Asp	Arg	Val	Leu 420	Asn	Phe	Leu	Lys	Asp 425	His	Phe	Leu	Met	Asp 430	Gly	Gln
Val	Arg	Ser 435	Arg	Met	Leu	Leu	Leu 440	Gln	Pro	Gln	Ala	Arg 445	Tyr	Gln	Arg
Val	Ala 450	Val	His	Arg	Val	Pro 455	Gly	Leu	His	His	Thr 460	Tyr	Asp	Val	Leu
Phe 465	Leu	Gly	Thr	Gly	Asp 470	Gly	Arg	Leu	His	Lys 475	Ala	Val	Ser	Val	Gly 480
Pro	Arg	Val	His	Ile 485	Ile	Glu	Glu	Leu	Gln 490	Ile	Phe	Ser	Ser	Gly 495	Gln
Pro	Val	Gln	Asn 500	Leu	Leu	Leu	Asp	Thr 505	His	Arg	Gly	Leu	Leu 510	Tyr	Ala
Ala	Ser	His 515	Ser	Gly	Val	Val	Gln 520	Val	Pro	Met	Ala	Asn 525	Cys	Ser	Leu
Tyr	Arg 530	Ser	Cys	Gly	Asp	Cys 535		Leu	Ala	Arg	Asp 540	Pro	Tyr	Cys	Ala
Trp 545	Ser	Gly	Ser	Ser	Cys 550		His	Val	Ser	Leu 555	Tyr	Gln	Pro	Gln	Leu 560
Ala	Thr	Arg	Pro	Trp 565		Gln	Asp	Ile	Glu 570		Ala	Ser	Ala	Lys 575	Asp
Leu	Cys	Ser	Ala 580		Ser	Val	Val	Ser 585		Ser	Phe	Val	Pro 590	Thr	Gly
Glu	Lys	Pro 595		Glu	Gln	Val	G1n 600		Gln	Pro	Asn	Thr 605		Asn	Thr
Leu	Ala		Pro	Leu	Leu	Ser 615		Leu	Ala	Thr	Arg 620		Trp	Leu	Arg
Asn 625		Ala	Pro	Val	Asn 630		Ser	Ala	Ser	Cys		Val	Leu	Pro	Thr 640
Gly	Asp	Leu	ı Leu	Leu 645		Gly	Thr	Gln	650		Gly	Glu	Phe	Gln 655	Cys
Trp	Ser	Leu	a Glu 660		ı Gly	? Phe	e Glm	Glr 665		ı Val	Ala	Ser	Tyr 670		Pro
Glı	ı Val	Val		ı Asp	Gly	/ Va]	Ala 680		Glr	n Thr	Asp	685 685		Gly	Ser
Va]	Pro 690	Val		e Ile	e Sei	Thi	Ser		g Val	l Sei	700		Ala	Gly	Gly
lve			r Tri	n Gla	v Ala			. Sei	r Tvi	r Tri	Lys	s Glu	ı Phe	e Lei	ı Val

705					710		•			715					720
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	Leu
				725					730					735	
Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	Gly	Glu
			740					745					750		
Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	Pro	Pro	Glu
		755					760					765			
Thr	Arg	Pro	Leu	Asn	Gly	Ļeu	Gly	Pro	Pro	Ser	Thr	Pro	Leu	Asp	His
	770					775					780				
Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	Gly	Ser	Arg	Val	Phe
785	÷				790					795					800
Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	Gln	Asp	Ser	Phe	Val	Glu
				805					810					815	
Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	Val	Arg	Leu	Gly	Ser	Glu	Ile
			820					825					830		
Arg	Asp	Ser	Val	Val											
		835													
<210)> 2														

<211> 2511

<212> DNA

<213> Human

<400> 2

atgctgcgca ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 60 120 cctcggccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc gccgcctccg 180 ${\tt acctgggcgc\ tcagccccg\ gatcagcctg\ cctctgggct\ ctgaagagcg\ gccattcctc}$ 240 agattcgaag ctgaacacat ctccaactac acagcccttc tgctgagcag ggatggcagg 300 accetgtacg tgggtgctcg agaggccctc tttgcactca gtagcaacct cagettcctg 360 ccaggcgggg agtaccagga gctgctttgg ggtgcagacg cagagaagaa acagcagtgc 420 agetteaagg geaaggacee acagegegae tgteaaaact acateaagat ceteetgeeg 480 ctcagcggca gtcacctgtt cacctgtggc acagcagcct tcagccccat gtgtacctac 540 atcaacatgg agaacttcac cctggcaagg gacgagaagg ggaatgtcct cctggaagat 600 ggcaagggcc gttgtccctt cgacccgaat ttcaagtcca ctgccctggt ggttgatggc 660 gagctctaca ctggaacagt cagcagcttc caagggaatg acccggccat ctcgcggagc 720 caaagccttc gccccaccaa gaccgagagc tccctcaact ggctgcaaga cccagctttt

gtggcctcag	cctacattcc	tgagagcctg	ggcagcttgc	aaggcgatga	tgacaagatc	780
	tcagcgagac					840
cgcattgccc	gcatctgcaa	gggcgatgag	ggtggagagc	gggtgctaca	gcagcgctgg	900
	tcaaggccca					960
gtgctgcagg	atgtcttcac	gctgagcccc	agcccccagg	actggcgtga	cacccttttc	1020
tatggggtct	tcacttccca	gtggcacagg	ggaactacag	aaggctctgc	cgtctgtgtc	1080
ttcacaatga	aggatgtgca	gagagtcttc	agcggcctct	acaaggaggt	gaaccgtgag	1140
acacagcaga	tggtacaccg	tgacccaccc	gtgcccacac	cccggcctgg	agcgtgcatc	1200
accaacagtg	cccgggaaag	gaagatcaac	tcatccctgc	agctcccaga	ccgcgtgctg	1260
aactttctca	aggaccactt	cctgatggac	gggcaggtcc	gaagccgcat	gctgctgctg	1320
cagccccagg	ctcgctacca	gcgcgtggct	gtacaccgcg	tccctggcct	gcaccacacc	1380
tacgatgtcc	tcttcctggg	cactggtgac	ggccggctcc	acaaggcagt	gagcgtgggc	1440
ccccgggtgc	acatcattga	ggagctgcag	atcttctcat	cgggacagcc	cgtgcagaat	1500
ctgctcctgg	acacccacag	ggggctgctg	tatgcggcct	cacactcggg	cgtagtccag	1560
gtgcccatgg	ccaactgcag	cctgtaccgg	agctgtgggg	actgcctcct	cgcccgggac	1620
ccctactgtg	cttggagcgg	ctccagctgc	aagcacgtca	gcctctacca	gcctcagctg	1680
gccaccaggc	cgtggatcca	ggacatcgag	ggagccagcg	ccaaggacct	ttgcagcgcg	1740
tcttcggttg	tgtccccgtc	ttttgtacca	acaggggaga	agccatgtga	gcaagtccag	1800
ttccagccca	acacagtgaa	cactttggcc	tgcccgctcc	tctccaacct	ggcgacccga	1860
ctctggctac	gcaacggggc	ccccgtcaat	gcctcggcct	cctgccacgt	gctacccact	1920
ggggacctgc	tgctggtggg	cacccaacag	ctgggggagt	tccagtgctg	gtcactagag	1980
gagggcttcc	agcagctggt	agccagctac	tgcccagagg	tggtggagga	cggggtggca	2040
gaccaaacag	atgagggtgg	cagtgtaccc	gtcattatca	gcacatcgcg	tgtgagtgca	2100
ccagctggtg	gcaaggccag	ctggggtgca	gacaggtcct	actggaagga	gttcctggtg	2160
atgtgcacgc	tctttgtgct	ggccgtgctg	ctcccagttt	tattcttgct	ctaccggcac	2220
cggaacagca	tgaaagtctt	cctgaagcag	ggggaatgtg	ccagcgtgca	ccccaagacc	2280
tgccctgtgg	tgctgcccc	tgagacccgc	ccactcaacg	gcctagggcc	ccctagcacc	2340
ccactcgatc	accgagggta	ccagtccctg	tcagacagcc	ccccggggtc	ccgagtcttc	2400
actgagtcag	agaagaggcc	actcagcatc	caagacagct	tcgtggaggt	atccccagtg	2460
tgcccccggc	cccgggtccg	ccttggctcg	gagatccgtg	actctgtggt	g	2511

<211> 3766

<212> DNA

<213> Human

```
60
gctctgccca agccgaggct gcggggccgg cgccggcggg aggactgcgg tgccccgcgg
aggggctgag tttgccaggg cccacttgac cctgtttccc acctcccgcc ccccaggtcc
                                                                     120
ggaggcgggg gcccccgggg cgactcgggg gcggaccgcg gggcggagct gccgccgtg
                                                                     180
agtccggccg agccacctga gcccgagccg cgggacaccg tcgctcctgc tctccgaatg
                                                                     240
                                                                     300
ctgcgcaccg cgatgggcct gaggagctgg ctcgccgccc catgggggcgc gctgccgcct
                                                                     360
cggccaccgc tgctgctgct cctgctgctg ctgctcctgc tgcagccgcc gcctccgacc
tgggcgctca gcccccggat cagcctgcct ctgggctctg aagagcggcc attcctcaga
                                                                     420
ttcgaagctg aacacatctc caactacaca gcccttctgc tgagcaggga tggcaggacc
                                                                     480
                                                                     540
ctgtacgtgg gtgctcgaga ggccctcttt gcactcagta gcaacctcag cttcctgcca
                                                                     600
ggcggggagt accaggagct gctttggggt gcagacgcag agaagaaaca gcagtgcagc
                                                                     660
ttcaagggca aggacccaca gcgcgactgt caaaactaca tcaagatcct cctgccgctc
                                                                     720
agcggcagtc acctgttcac ctgtggcaca gcagccttca gccccatgtg tacctacatc
                                                                     780
aacatggaga acttcaccct ggcaagggac gagaagggga atgtcctcct ggaagatggc
                                                                     840
aagggccgtt gtcccttcga cccgaatttc aagtccactg ccctggtggt tgatggcgag
                                                                     900
ctctacactg gaacagtcag cagcttccaa gggaatgacc cggccatctc gcggagccaa
                                                                     960
agcettegee ceaceaagae egagagetee eteaactgge tgeaagaeee agettttgtg
                                                                    1020
gcctcagcct acattcctga gagcctgggc agcttgcaag gcgatgatga caagatctac
tttttcttca gcgagactgg ccaggaattt gagttctttg agaacaccat tgtgtcccgc
                                                                    1080
                                                                    1140
attgcccgca tctgcaaggg cgatgagggt ggagagcggg tgctacagca gcgctggacc
                                                                    1200
tccttcctca aggcccagct gctgtgctca cggcccgacg atggcttccc cttcaacgtg
                                                                     1260
ctgcaggatg tcttcacgct gagccccagc ccccaggact ggcgtgacac ccttttctat
                                                                    1320
ggggtcttca cttcccagtg gcacagggga actacagaag gctctgccgt ctgtgtcttc
acaatgaagg atgtgcagag agtcttcagc ggcctctaca aggaggtgaa ccgtgagaca
                                                                     1380
                                                                     1440
cagcagatgg tacaccgtga cccacccgtg cccacacccc ggcctggagc gtgcatcacc
aacagtgccc gggaaaggaa gatcaactca tccctgcagc tcccagaccg cgtgctgaac
                                                                     1500
                                                                     1560
tttctcaagg accacttcct gatggacggg caggtccgaa gccgcatgct gctgctgcag
                                                                     1620
ccccaggete getaccageg egtggetgta cacegegtee etggeetgea ccacacetae
gatgtcctct tcctgggcac tggtgacggc cggctccaca aggcagtgag cgtgggcccc
                                                                     1680
                                                                     1740
cgggtgcaca tcattgagga gctgcagatc ttctcatcgg gacagcccgt gcagaatctg
ctcctggaca cccacagggg gctgctgtat gcggcctcac actcgggcgt agtccaggtg
                                                                     1800
                                                                     1860
cccatggcca actgcagcct gtaccggagc tgtggggact gcctcctcgc ccgggacccc
                                                                     1920
 tactgtgctt ggagcggctc cagctgcaag cacgtcagcc tctaccagcc tcagctggcc
                                                                     1980
 accaggccgt ggatccagga catcgaggga gccagcgcca aggacctttg cagcgcgtct
 tcggttgtgt ccccgtcttt tgtaccaaca ggggagaagc catgtgagca agtccagttc
                                                                     2040
 cagcccaaca cagtgaacac tttggcctgc ccgctcctct ccaacctggc gacccgactc
                                                                     2100
 tggctacgca acggggcccc cgtcaatgcc tcggcctcct gccacgtgct acccactggg
                                                                     2160
```

2220 gacctgctgc tggtgggcac ccaacagctg ggggagttcc agtgctggtc actagaggag 2280 ggcttccagc agctggtagc cagctactgc ccagaggtgg tggaggacgg ggtggcagac 2340 caaacagatg agggtggcag tgtacccgtc attatcagca catcgcgtgt gagtgcacca gctggtggca aggccagctg gggtgcagac aggtcctact ggaaggagtt cctggtgatg 2400 2460 tgcacgctct ttgtgctggc cgtgctgctc ccagttttat tcttgctcta ccggcaccgg aacagcatga aagtcttcct gaagcagggg gaatgtgcca gcgtgcaccc caagacctgc 2520 2580 cctgtggtgc tgcccctga gacccgcca ctcaacggcc tagggccccc tagcacccca 2640 ctcgatcacc gagggtacca gtccctgtca gacagccccc cggggtcccg agtcttcact 2700 gagtcagaga agaggccact cagcatccaa gacagcttcg tggaggtatc cccagtgtgc 2760 ccccggcccc gggtccgcct tggctcggag atccgtgact ctgtggtgtg agagctgact 2820 tccagaggac gctgccctgg cttcaggggc tgtgaatgct cggagagggt caactggacc 2880 teceeteege tetgetette gtggaacaeg accgtggtge eeggeeettg ggageettgg 2940 ggccagctgg cctgctgctc tccagtcaag tagcgaagct cctaccaccc agacacccaa acagccgtgg ccccagaggt cctggccaaa tatgggggcc tgcctaggtt ggtggaacag 3000 tgctccttat gtaaactgag ccctttgttt aaaaaaacaat tccaaatgtg aaactagaat 3060 3120 gagagggaag agatagcatg gcatgcagca cacacggctg ctccagttca tggcctccca ggggtgctgg ggatgcatcc aaagtggttg tctgagacag agttggaaac cctcaccaac 3180 3240 tggcctcttc accttccaca ttatcccgct gccaccggct gccctgtctc actgcagatt caggaccagc ttgggctgcg tgcgttctgc cttgccagtc agccgaggat gtagttgttg 3300 3360 ctgccgtcgt cccaccacct cagggaccag agggctaggt tggcactgcg gccctcacca ggtcctgggc tcggacccaa ctcctggacc tttccagcct gtatcaggct gtggccacac 3420 3480 gagaggacag cgcgagctca ggagagattt cgtgacaatg tacgcctttc cctcagaatt cagggaagag actgtcgcct gccttcctcc gttgttgcgt gagaacccgt gtgccccttc 3540 ccaccatatc caccctcgct ccatctttga actcaaacac gaggaactaa ctgcaccctg 3600 gtectetece cagtececag tteaccetee ateceteace tteetecact etaagggata 3660 3720 tcaacactgc ccagcacagg ggccctgaat ttatgtggtt tttatacatt ttttaataag 3766 atgcacttta tgtcattttt taataaagtc tgaagaatta ctgttt

<210> 4

<211> 837

<212> PRT

<213> Human

<400> 4

Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro Trp

5

									8	/30					
Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu
			20					25					30		
Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser	Pro	Arg	Ile
		35					40					45			
Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe		Arg	Phe	Glu	Ala
	50					55					60				
Glu	His	Ile	Ser	Asn		Thr	Ala	Leu	Leu		Ser	Arg	Asp	Gly	Arg
65					70					75			_		80
Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala		Phe	Ala	Leu	Ser		Asn
				85	0.1	61	0.1	T	90	0.1	,	,	T.	95	47.
Leu	Ser	Phe		Pro	Gly	Gly	GIU		GIN	GIU	Leu	Leu		GIY	Ala
۸	41 a	C1	100	1	Cln	C1 n	Cva	105	Dha	Lvc	Gl _v	lvc	110	Pro	Gln.
ASP	на	115	Lys	Lys	GIN	GIII	120	Sei	riie	Lys	Oly	125	лър	110	0111
Δra	Δen		Gln	Asn	Tyr	Ile		Πe	Len	Len	Pro		Ser	Glv	Ser
	130	Cys	OIII	лы	1 9 1	135	Lys	110	Leu	Leu	140	Deu	501	01)	561
		Phe	Thr	Cys	G1v		Ala	Ala	Phe	Ser		Met	Cvs	Thr	Tyr
145	Lou	1110	****	0,0	150	****				155			- , -		160
	Asn	Met	Glu	Asn		Thr	Leu	Ala	Arg		Glu	Lys	Gly	Asn	Val
				165					170					175	
Leu	Leu	Glu	Asp	Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys
			180					185					190		
Ser	Thr	Ala	Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ile
		195					200					205			
Ser	Phe	Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	G1n	Ser	Leu	Arg
	210					215					220				
	Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn			Gln	Asp	Pro	Ala	
225					230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser		Gly	Ser	Leu	Gln		Asp
				245	D.	D)	D.		250	T)	0.3	0.3	01	255 Di	C1
Asp	Asp	Lys		Tyr	Phe	Phe	Phe		Glu	Thr	Gly	GIn		Phe	Glu
ים	Di.	C1	260	T1.	71.	W - 1	C	265	T1 -	A1 =	۸	т1 -	270	1	C1
rne	rne		Asn	Thr	11e	val		Arg	11e	мта	Arg		cys	Lys	GIÀ
Δ α ~	G1	275	61	G1	Δ~~	Val	280	G15	Gla	Ara	Trr	285 Thr	Sor	Phe	الم [
изр	290	GIY	GIÀ	Glu	viß	va1 295	Leu	OIII	GIII	vi g	300		261	1 116	Leu
lve		Gln	ا وا	Leu	Cve		Arø	Pro	Asn	Asn			Pro	Phe	Asn
Lys	MIG	0111	Leu	Leu	Uys	061	ni B	110	usb	,,sp	O I y	1 110	. 10		1.011

305					310					315					320
Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro	Ser	Pro	Gln	Asp	Trp	Arg
				325					330					335	
Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr	Ser	Gln	Trp	His	Arg	Gly	Thr
			340					345					350		
Thr	Glu	Gly	Ser	Ala	Val	Cys	Val	Phe	Thr	Met	Lys	Asp	Val	Gln	Arg
		355					360					365			
Val	Phe	Ser	Gly	Leu	Tyr	Lys	Glu	Val	Asn	Arg	Glu	Thr	Gln	Gln	Met
	370					375					380				
Val	His	Arg	Asp	Pro	Pro	Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile
385					390					395					400
Thr	Asn	Ser	Ala	Arg	Glu	Arg	Lys	Ile	Asn	Ser	Ser	Leu	Gln	Leu	Pro
				405					410					415	
Asp	Arg	Val	Leu	Asn	Phe	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln
			420					425					430		
Val	Arg	Ser	Arg	Met	Leu	Leu	Leu	Gln	Pro	Gln	Ala	Arg	Tyr	Gln	Arg
		435					440					445			
Val	Ala	Val	His	Arg	Val	Pro	Gly	Leu	His	His	Thr	Tyr	Asp	Val	Leu
	450					455					460				
Phe	Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly
465					470					475					480
Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly	Gln
				485					490					495	
Pro	Val	Gln		Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu	Tyr	Ala
			500					505					510		
Ala	Ser	His	Ser	Gly	Val	Val			Pro	Met	Ala		Cys	Ser	Leu
		515					520					525	_	_	
Tyr		Ser	Cys	Gly	Asp		Leu	Leu	Ala	Arg		Pro	Tyr	Cys	Ala
_	530		_	_		535			_	_	540		_	0.1	
	Ser	Gly	Ser	Ser		Lys	His	Val	Ser	Leu	Tyr	GIn	Pro	Gln	
545			_	_	550			~ .		555		_			560
Ala	Thr	Arg	Pro		He	GIn	Asp	lle		Gly	Ala	Ser	Ala		Asp
		_		565	_			_	570		n.		n	575	0.1
Leu	Cys	Ser		Ser	Ser	Val	Val		Pro	Ser	Phe	Val		Ihr	Gly
6.1	,	n	580	63	01	17 1	0.1	585	61	n.		TI	590		TI
Glu	Lys		Cys	GIU	GIN	val		rne	GIN	Pro	ASN		vaı	Asn	ınr
		595					600					605			

Leu	Ala	Cys	Pro	Leu	Leu		Asn	Leu	Ala	Thr		Leu	Trp	Leu	Arg
	610					615					620				
Asn	Gly	Ala	Pro	Val	Asn	Ala	Ser	Ala	Ser	Cys	His	Val	Leu	Pro	Thr
625					630					635					640
Gly	Asp	Leu	Leu	Leu	Val	Gly	Thr	Gln	Gln	Leu	Gly	Glu	Phe	Gln	Cys
		•		645					650					655	
Trp	Ser	Leu	Glu	Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro
			660					665					670		
Glu	Val	Val	Glu	Asp	G1y	Val	Ala	Asp	Gln	Thr	Asp	Glu	Gly	Gly	Ser
		675					680					685			
Val	Pro	Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly
	690					695					700				
Lys	Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val
705					710					715					720
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	Leu
				725					730					735	
Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	Gly	Glu
			740					745					750		
Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	Pro	Pro	Glu
		755	I				760					765			
Thr	Arg	Pro	Leu	Asn	Gly	Leu	G1y	Pro	Pro	Ser	Thr	Pro	Leu	Asp	His
	770)				775					780)			
Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	Gly	Ser	Arg	Val	Phe
785					790					795					800
Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	· Ile	Glr	Asp	Ser	Phe	Val	Glu
				805					810					815	
Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	y Val	Are	g Lei	ı Gly	Ser	Glu	Ile
			820					825					830		
Arg	g Asr	Sei	· Val	Val											
		835						•							

<211> 2511

<212> DNA

<213> Human

atgctgcgca	ccgcgatggg	cctgaggagc	tggctcgccg	ccccatgggg	cgcgctgccg	60
cctcggccac	cgctgctgct	gctcctgcta	ctgctgctcc	tgctgcagcc	accgcctccg	120
acctgggcgc	tcagcccccg	gatcagcctg	cctctgggct	ctgaagagcg	gccattcctc	180
agattcgaag	ctgaacacat	ctccaactac	acagcccttc	tgctgagcag	ggatggcagg	240
accctgtacg	tgggtgctcg	agaggccctc	tttgcactca	gtagcaacct	cagcttcctg	300
ccaggcgggg	agtaccagga	gctgctttgg	ggtgcagacg	cagagaagaa	acagcagtgc	360
agcttcaagg	gcaaggaccc	acagcgcgac	tgtcaaaact	acatcaagat	cctcctgccg	420
ctcagcggca	gtcacctgtt	cacctgtggc	acagcagcct	tcagccccat	gtgtacctac	480
atcaacatgg	agaacttcac	cctggcaagg	gacgagaagg	ggaatgtcct	cctggaagat	540
ggcaagggcc	gttgtccctt	cgacccgaat	ttcaagtcca	ctgccctggt	ggttgatggc	600
gagctctaca	ctggaacagt	catcagcttc	caagggaatg	acccggccat	ctcgcggagc	660
caaagccttc	gccccaccaa	gaccgagagc	tccctcaact	ggctgcaaga	cccagctttt	720
gtggcctcag	cctacattcc	tgagagcctg	ggcagcttgc	aaggcgatga	tgacaagatc	780
tactttttct	tcagcgagac	tggccaggaa	tttgagttct	ttgagaacac	cattgtgtcc	840
cgcattgccc	gcatctgcaa	gggcgatgag	ggtggagagc	gggtgctaca	gcagcgctgg	900
acctccttcc	tcaaggccca	gctgctgtgc	tcacggcccg	acgatggctt	ccccttcaac	960
gtgctgcagg	atgtcttcac	gctgagcccc	agcccccagg	actggcgtga	cacccttttc	1020
tatggggtct	tcacttccca	gtggcacagg	ggaactacag	aaggctctgc	cgtctgtgtc	1080
ttcacaatga	aggatgtgca	gagagtcttc	agcggcctct	acaaggaggt	gaaccgtgag	1140
acacagcaga	tggtacaccg	tgacccaccc	gtgcccacac	cccggcctgg	agcgtgcatc	1200
accaacagtg	cccgggaaag	gaagatcaac	tcatccctgc	agctcccaga	ccgcgtgctg	1260
aactttctca	aggaccactt	cctgatggac	gggcaggtcc	gaagccgcat	gctgctgctg	1320
cagccccagg	ctcgctacca	gcgcgtggct	gtacaccgcg	tccctggcct	gcaccacacc	1380
tacgatgtcc	tcttcctggg	cactggtgac	ggccggctcc	acaaggcagt	gagcgtgggc	1440
ccccgggtgc	acatcattga	ggagctgcag	atcttctcat	cgggacagcc	cgtgcagaat	1500
				cacactcggg		1560
gtgcccatgg	ccaactgcag	cctgtaccgg	agctgtgggg	actgcctcct	cgcccgggac	1620
				gcctctacca		1680
				ccaaggacct		1740
tcttcggttg	tgtccccgtc	ttttgtacca	acaggggaga	agccatgtga	gcaagtccag	1800
ttccagccca	acacagtgaa	cactttggcc	tgcccgctcc	tctccaacct	ggcgacccga	1860
				cctgccacgt		1920
					gtcactagag	1980
					cggggtggca	2040
					tgtgagtgca	2100
ccagctggtg	gcaaggccag	ctggggtgca	a gacaggtcct	actggaagga	gttcctggtg	2160

atgtgcacgc	tctttgtgct	ggccgtgctg	ctcccagttt	tattcttgct	ctaccggcac	2220
cggaacagca	tgaaagtctt	cctgaagcag	ggggaatgtg	ccagcgtgca	ccccaagacc	2280
tgccctgtgg	tgctgccccc	tgagacccgc	ccactcaacg	gcctagggcc	ccctagcacc	2340
ccactcgatc	accgagggta	ccagtccctg	tcagacagcc	ccccggggtc	ccgagtcttc	2400
actgagtcag	agaagaggcc	actcagcatc	caagacagct	tcgtggaggt	atccccagtg	2460
tgccccggc	cccgggtccg	ccttggctcg	gagatccgtg	actctgtggt	g	2511

<211> 3766

<212> DNA

<213> Human

gctctgccca	agccgaggct	gcggggccgg	cgccggcggg	aggactgcgg	tgccccgcgg	60
aggggctgag	tttgccaggg	cccacttgac	cctgtttccc	acctcccgcc	ccccaggtcc	120
ggaggcgggg	gccccgggg	cgactcgggg	gcggaccgcg	gggcggagct	gccgcccgtg	180
agtccggccg	agccacctga	gcccgagccg	cgggacaccg	tcgctcctgc	tctccgaatg	240
ctgcgcaccg	cgatgggcct	gaggagctgg	ctcgccgccc	catggggcgc	gctgccgcct	300
cggccaccgc	tgctgctgct	cctgctactg	ctgctcctgc	tgcagccacc	gcctccgacc	360
tgggcgctca	gccccggat	cagcctgcct	ctgggctctg	aagagcggcc	attcctcaga	420
ttcgaagctg	aacacatctc	caactacaca	gcccttctgc	tgagcaggga	tggcaggacc	480
ctgtacgtgg	gtgctcgaga	ggccctcttt	gcactcagta	gcaacctcag	cttcctgcca	540
ggcggggagt	accaggagct	gctttggggt	gcagacgcag	agaagaaaca	gcagtgcagc	600
ttcaagggca	aggacccaca	gcgcgactgt	caaaactaca	tcaagatcct	cctgccgctc	660
agcggcagtc	acctgttcac	ctgtggcaca	gcagccttca	gccccatgtg	tacctacatc	720
aacatggaga	acttcaccct	ggcaagggac	gagaagggga	atgtcctcct	ggaagatggc	780
aagggccgtt	gtcccttcga	cccgaatttc	aagtccactg	ccctggtggt	tgatggcgag	840
ctctacactg	gaacagtcat	cagcttccaa	gggaatgacc	cggccatctc	gcggagccaa	900
agccttcgcc	ccaccaagac	cgagagctcc	ctcaactggc	tgcaagaccc	agcttttgtg	960
gcctcagcct	acattcctga	gagcctgggc	agcttgcaag	gcgatgatga	caagatctac	1020
tttttcttca	gcgagactgg	ccaggaattt	gagttctttg	agaacaccat	tgtgtcccgc	1080
attgcccgca	tctgcaaggg	cgatgagggt	ggagagcggg	tgctacagca	gcgctggacc	1140
tccttcctca	aggcccagct	gctgtgctca	cggcccgacg	atggcttccc	cttcaacgtg	1200
ctgcaggatg	tcttcacgct	gagccccagc	ccccaggact	ggcgtgacac	ccttttctat	1260
ggggtcttca	cttcccagtg	gcacagggga	actacagaag	gctctgccgt	ctgtgtcttc	1320
acaatgaagg	atgtgcagag	agtcttcagc	ggcctctaca	aggaggtgaa	ccgtgagaca	1380

cagcagatgg	tacaccgtga	cccacccgtg	cccacacccc	ggcctggagc	gtgcatcacc	1440
aacagtgccc	gggaaaggaa	gatcaactca	tccctgcagc	tcccagaccg	cgtgctgaac	1500
tttctcaagg	accacttcct	gatggacggg	caggtccgaa	gccgcatgct	gctgctgcag	1560
ccccaggctc	gctaccagcg	cgtggctgta	caccgcgtcc	ctggcctgca	ccacacctac	1620
gatgtcctct	tcctgggcac	tggtgacggc	cggctccaca	aggcagtgag	cgtgggcccc	1680
cgggtgcaca	tcattgagga	gctgcagatc	ttctcatcgg	gacagcccgt	gcagaatctg	1740
ctcctggaca	cccacagggg	gctgctgtat	gcggcctcac	actcgggcgt	agtccaggtg	1800
cccatggcca	actgcagcct	gtaccggagc	tgtggggact	gcctcctcgc	ccgggacccc	1860
tactgtgctt	ggagcggctc	cagctgcaag	cacgtcagcc	tctaccagcc	tcagctggcc	1920
accaggccgt	ggatccagga	catcgaggga	gccagcgcca	aggacctttg	cagcgcgtct	1980
tcggttgtgt	ccccgtcttt	tgtaccaaca	ggggagaagc	catgtgagca	agtccagttc	2040
cagcccaaca	cagtgaacac	tttggcctgc	ccgctcctct	ccaacctggc	gacccgactc	2100
tggctacgca	acggggcccc	cgtcaatgcc	tcggcctcct	gccacgtgct	acccactggg	2160
gacctgctgc	tggtgggcac	ccaacagctg	ggggagttcc	agtgctggtc	actagaggag	2220
ggcttccagc	agctggtagc	cagctactgc	ccagaggtgg	tggaggacgg	ggtggcagac	2280
caaacagatg	agggtggcag	tgtacccgtc	attatcagca	catcgcgtgt	gagtgcacca	2340
gctggtggca	aggccagctg	gggtgcagac	aggtcctact	ggaaggagtt	cctggtgatg	2400
tgcacgctct	ttgtgctggc	cgtgctgctc	ccagttttat	tcttgctcta	ccggcaccgg	2460
aacagcatga	aagtcttcct	gaagcagggg	gaatgtgcca	gcgtgcaccc	caagacctgc	2520
cctgtggtgc	tgccccctga	gacccgccca	ctcaacggcc	tagggccccc	tagcacccca	2580
ctcgatcacc	gagggtacca	gtccctgtca	gacagccccc	cggggtcccg	agtcttcact	2640
gagtcagaga	agaggccact	cagcatccaa	gacagcttcg	tggaggtatc	cccagtgtgc	2700
ccccggcccc	gggtccgcct	tggctcggag	atccgtgact	ctgtggtgtg	agagctgact	2760
tccagaggac	gctgccctgg	cttcaggggc	tgtgaatgct	cggagagggt	caactggacc	2820
tccctccgc	tctgctcttc	gtggaacacg	accgtggtgc	ccggcccttg	ggagccttgg	2880
ggccagctgg	cctgctgctc	tccagtcaag	tagcgaagct	cctaccaccc	agacacccaa	2940
acagccgtgg	ccccagaggt	cctggccaaa	tatgggggcc	tgcctaggtt	ggtggaacag	3000
tgctccttat	gtaaactgag	ccctttgttt	aaaaaacaat	tccaaatgtg	aaactagaat	3060
gagagggaag	agatagcatg	gcatgcagca	cacacggctg	ctccagttca	tggcctccca	3120
ggggtgctgg	ggatgcatcc	aaagtggttg	tctgagacag	agttggaaac	cctcaccaac	3180
tggcctcttc	accttccaca	ttatcccgct	gccaccggct	gccctgtctc	actgcagatt	3240
caggaccagc	ttgggctgcg	tgcgttctgc	cttgccagtc	agccgaggat	gtagttgttg	3300
ctgccgtcgt	cccaccacct	cagggaccag	agggctaggt	tggcactgcg	gccctcacca	3360
ggtcctgggc	tcggacccaa	ctcctggacc	tttccagcct	gtatcaggct	gtggccacac	3420
gagaggacag	cgcgagctca	ggagagattt	cgtgacaatg	tacgcctttc	cctcagaatt	3480
cagggaagag	actgtcgcct	gccttcctcc	gttgttgcgt	gagaacccgt	gtgccccttc	3540
ccaccatatc	caccctcgct	ccatctttga	actcaaacac	gaggaactaa	ctgcaccctg	3600

gtcctctccc cagtccccag ttcaccctcc atccctcacc ttcctccact ctaagggata	a
tcaacactgc ccagcacagg ggccctgaat ttatgtggtt tttatacatt ttttaataag	
atgcacttta tgtcattttt taataaagtc tgaagaatta ctgttt	_
atgedettta tgtedetttt taataagse tgasgerin ison	
<210> 7	
<211> 837	
<212> PRT	
<213> Human	
<400> 7	
Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro Trp	
5 10 15	
Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu Leu	
20 25 30	
Leu Leu Cln Pro Pro Pro Pro Thr Trp Ala Leu Ser Pro Arg Ile	
35 40 45	
Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu Arg Phe Glu Ala	
50 55 60	
Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu Ser Arg Asp Gly Arg	
65 70 75 80	
Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Leu Ser Ser Asn	
85 90 95	
Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala	
100 105 110	
Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys Gly Lys Asp Pro Gln	
115 120 125	
Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu Pro Leu Ser Gly Ser	
130 135 140	
His Leu Phe Thr Cys Gly Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr 145 150 155 160	
145 150 155 160 Ile Asn Ile Glu Asn Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val	
THE ASSETT OF THE ASSET OF THE LEG MIN ALE ASSET ON LINE AND UTT	

Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys

Ser Thr Ala Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser

. 180

Ser		Gln	Gly	Asn	Asp		Ala	Ile	Ser	Arg		GIn	Ser	Leu	Arg
	210					215					220		_		D .
Pro	Thr	Lys	Thr	Glu		Ser	Leu	Asn	Trp		Gln	Asp	Pro	Ala	
225					230					235		_			240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser		Gly	Ser	Leu	Gln		Asp
				245					250					255	
Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe		Glu	Thr	Gly	Gln		Phe	Glu
			260					265					270	_	
Phe	Phe	Glu	Asn	Thr	Ile	Val		Arg	Ile	Ala	Arg		Cys	Lys	Gly
		275					280				_	285	_		
Asp		Gly	Gly	Glu	Arg		Leu	Gln	Gln	Arg		Thr	Ser	Phe	Leu
	290					295		_			300		_	D.	
Lys	Ala	Gln	Leu	Leu		Ser	Arg	Pro	Asp		Gly	Phe	Pro	Phe	
305					310				_	315					320
Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser		Ser	Pro	GIn	Asp		Arg
				325					330		_			335	mı
Asp	Thr	Leu		Tyr	Gly	Val	Phe		Ser	Gln	Trp	His		Gly	Thr
			340					345			-		350	0.1	
Thr	Glu		Ser	Ala	Val	Cys		Phe	Thr	Met	Lys		Val	GIn	Arg
		355			_		360				0.1	365	0.1	0.1	M
Val			Gly	Leu	Tyr		Glu	Val	Asn	Arg		lhr	GIn	GIn	мет
	370			-	_	375		m.	Б		380	01	4.1	C	т1.
	His	Arg	Asp	Pro		Val	Pro	Thr	Pro		Pro	GIY	Ala	Cys	
385					390					395	C	,	01	T	400 D
Thr	Asn	Ser	Ala	Arg	Glu	Arg	Lys	He			Ser	Leu	GIN		Pro
			_	405	D.	,	,		410		1	W.4	۸	415	C1
Asp	Arg	Val		Asn	Phe	Leu	Lys		Hls	Pne	Leu	мет			GIII
		0	420			,		425	D	C1	۸٦.	۸	430		A 20 00
Val	Arg			Met	Leu	Leu		GIN	Pro	GIN	на	445		GIII	Arg
., 1		435				D	440	ĭ	112 -	u.	Tha			Vol.	Lou
Val			HIS	Arg	val			Leu	пis	піѕ	460		ASp	val	Leu
ъ.	450		T)	0.1		455		1	112 -	1			Con	. Val	Cl _w
		Gly	Thr	Gly			Arg	Leu	HIS			vai	Ser	val	Gly
465		37.3	,,,,		470		C1	1	C1	475		C		C1	480
Pro	Arg	; Val	His	Ile		Glu	Glu	Leu			rne	ser	ser		
_				485				Tr.	490		61	. 1	. 1	495	
Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	lhr	His	Arg	Gly	Leu	Leu	ııyr	Ala

			500					505					510		
Ala	Ser	His	Ser	Gly	Val	Val	Gln	Val	Pro	Met	Ala	Asn	Cys	Ser	Leu
		515					520					525			
Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala
	530					535					540				
Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu	Tyr	Gln	Pro	Gln	Leu
545					550					555					560
Ala	Thr	Arg	Pro	Trp	Ile	Gln	Asp	Ile	Glu	Gly	Ala	Ser	Ala	Lys	Asp
				565					570					575	
Leu	Cys	Ser	Ala	Ser	Ser	Val	Val	Ser	Pro	Ser	Phe	Val	Pro	Thr	Gly
			580					585					590		
Glu	Lys	Pro	Cys	Glu	Gln	Val	Gln	Phe	Gln	Pro	Asn	Thr	Val	Asn	Thr
		595					600					605			
Leu	Ala	Cys	Pro	Leu	Leu	Ser	Asn	Leu	Ala	Thr	Arg	Leu	Trp	Leu	Arg
	610		•			615					620				
Asn	Gly	Ala	Pro	Val	Asn	Ala	Ser	Ala	Ser	Cys	His	Val	Leu	Pro	Thr
625					630					635					640
Gly	Asp	Leu	Leu	Leu	Val	Gly	Thr	Gln	Gln	Leu	Gly	Glu	Phe	Gln	Cys
				645					650					655	
Trp	Ser	Leu	Glu	Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro
			660					665					670		
Glu	Val	Val	Glu	Asp	Gly	Val	Ala	Asp	Gln	Thr	Asp	Glu	Gly	Gly	Ser
		675					680					685			
Val	Pro	Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	G1y
	690					695					700				
Lys	Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val
705					710					715					720
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu		Leu
				725					730					735	
Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	Gly	Glu
			740					745					750		
Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val		Pro	Pro	Glu
		755					760					765			
Thr	Arg	Pro	Leu	Asn	Gly		Gly	Pro	Pro	Ser	Thr	Pro	Leu	Asp	His
	770					775					780				
Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	Gly	Ser	Arg	Val	Phe
785					790					795					800

Arg Asp Ser Val Val 835

<210> 8 <211> 2511 <212> DNA

<213> Human

<400> 8

60 atgctgcgca ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 120 cctcggccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc gccgcctccg 180 acctgggcgc tcagccccg gatcagccta cctctgggct ctgaagagcg gccattcctc agattegaag etgaacacat etceaactae acageeette tgetgageag ggatggeagg 240 300 accetgtacg tgggtgeteg agaggeeete tttgeactea gtageaacct cagetteetg 360 ccaggcgggg agtaccagga gctgctttgg ggtgcagacg cagagaagaa acagcagtgc 420 agetteaagg geaaggacce acagegegae tgteaaaact acateaagat ceteetgeeg 480 ctcagcggca gtcacctgtt cacctgtggc acagcagcct tcagccccat gtgtacctac atcaacatag agaacttcac cctggcaagg gacgagaagg ggaatgttct cctggaagat 540 600 ggcaagggcc gttgtccctt cgacccgaat ttcaagtcca ctgccctggt ggttgatggc 660 gagctctaca ctggaacagt cagcagcttc caagggaatg acccggccat ctcgcggagc caaagcette geeceaceaa gaeegagage teeeteaact ggetgeaaga eecagetttt 720 780 gtggcctcag cctacattcc tgagagcctg ggcagcttgc aaggcgatga tgacaagatc 840 tactttttct tcagcgagac tggccaggaa tttgagttct ttgagaacac cattgtgtcc 900 cgcattgccc gcatctgcaa gggcgatgag ggtggagagc gggtgctaca gcagcgctgg 960 acctecttee teaaggeeca getgetgtge teaeggeecg acgatggett eccetteaac 1020 gtgctgcagg atgtcttcac gctgagcccc agcccccagg actggcgtga cacccttttc tatggggtct tcacttccca gtggcacagg ggaactacag aaggctctgc cgtctgtgtc 1080 ttcacaatga aggatgtgca gagagtcttc agcggcctct acaaggaggt gaaccgtgag 1140 1200 acacagcaga tggtacaccg tgacccaccc gtgcccacac cccggcctgg agcgtgcatc accaacagtg cccgggaaag gaagatcaac tcatccctgc agctcccaga ccgcgtgctg 1320 aacttectea aggaceactt eetgatggae gggeaggtee gaageegeat getgetgetg cagccccagg ctcgctacca gcgcgtggct gtacaccgcg tccctggcct gcaccacacc

tacgatgtcc	tcttcctggg	cactggtgac	ggccggctcc	acaaggcagt	gagcgtgggc	1440
ccccgggtgc	acatcattga	ggagctgcag	atcttctcat	cgggacagcc	cgtgcagaat	1500
ctgctcctgg	acacccacag	ggggctgctg	tatgcggcct	cacactcggg	cgtagtccag	1560
gtgcccatgg	ccaactgcag	cctgtacagg	agctgtgggg	actgcctcct	cgcccgggac	1620
ccctactgtg	cttggagcgg	ctccagctgc	aagcacgtca	gcctctacca	gcctcagctg	1680
gccaccaggc	cgtggatcca	ggacatcgag	ggagccagcg	ccaaggacct	ttgcagcgcg	1740
tcttcggttg	tgtccccgtc	ttttgtacca	acaggggaga	agccatgtga	gcaagtccag	1800
ttccagccca	acacagtgaa	cactttggcc	tgcccgctcc	tctccaacct	ggcgacccga	1860
ctctggctac	gcaacggggc	ccccgtcaat	gcctcggcct	cctgccacgt	gctacccact	1920
ggggacctgc	tgctggtggg	cacccaacag	ctgggggagt	tccagtgctg	gtcactagag	1980
gagggcttcc	agcagctggt	agccagctac	tgcccagagg	tggtggagga	cggggtggca	2040
gaccaaacag	atgagggtgg	cagtgtaccc	gtcattatca	gcacatcgcg	tgtgagtgca	2100
ccagctggtg	gcaaggccag	ctggggtgca	gacaggtcct	actggaagga	gttcctggtg	2160
atgtgcacgc	tctttgtgct	ggccgtgctg	ctcccagttt	tattcttgct	ctaccggcac	2220
cggaacagca	tgaaagtctt	cctgaagcag	ggggaatgtg	ccagcgtgca	ccccaagacc	2280
tgccctgtgg	tgctgccccc	tgagacccgc	ccactcaacg	gcctagggcc	ccctagcacc	2340
ccgctcgatc	accgagggta	ccagtccctg	tcagacagcc	ccccggggtc	ccgagtcttc	2400
actgagtcag	agaagaggcc	actcagcatc	caagacagct	tcgtggaggt	atccccagtg	2460
tgccccggc	cccgggtccg	ccttggctcg	gagatccgtg	actctgtggt	g	2511

<211> 3766

<212> DNA

<213> Human

gctctgccca	agccgaggct	gcggggccgg	cgccggcggg	aggactgcgg	tgccccgcgg	60
aggggctgag	tttgccaggg	cccacttgac	cctgtttccc	acctcccgcc	ccccaggtcc	120
ggaggcgggg	gccccgggg	cgactcgggg	gcggaccgcg	gggcggagct	gccgcccgtg	180
agtccggccg	agccacctga	gcccgagccg	cgggacaccg	tcgctcctgc	tctccgaatg	240
ctgcgcaccg	cgatgggcct	gaggagctgg	ctcgccgccc	catggggcgc	gctgccgcct	300
cggccaccgc	tgctgctgct	cctgctgctg	ctgctcctgc	tgcagccgcc	gcctccgacc	360
tgggcgctca	gcccccggat	cagcctacct	ctgggctctg	aagagcggcc	attcctcaga	420
ttcgaagctg	aacacatctc	caactacaca	gcccttctgc	tgagcaggga	tggcaggacc	480
ctgtacgtgg	gtgctcgaga	ggccctcttt	gcactcagta	gcaacctcag	cttcctgcca	540
ggcggggagt	accaggagct	gctttggggt	gcagacgcag	agaagaaaca	gcagtgcagc	600

	ttcaagggca	aggacccaca	gcgcgactgt	caaaactaca	tcaagatcct	cctgccgctc	660
	agcggcagtc	acctgttcac	ctgtggcaca	gcagccttca	gccccatgtg	tacctacatc	720
	aacatagaga	acttcaccct	ggcaagggac	gagaagggga	atgttctcct	ggaagatggc	780
	aagggccgtt	gtcccttcga	cccgaatttc	aagtccactg	ccctggtggt	tgatggcgag	840
•	ctctacactg	gaacagtcag	cagcttccaa	gggaatgacc	cggccatctc	gcggagccaa	900
	agccttcgcc	ccaccaagac	cgagagctcc	ctcaactggc	tgcaagaccc	agcttttgtg	960
	gcctcagcct	acattcctga	gagcctgggc	agcttgcaag	gcgatgatga	caagatctac	1020
	tttttcttca	gcgagactgg	ccaggaattt	gagttctttg	agaacaccat	tgtgtcccgc	1080
	attgcccgca	tctgcaaggg	cgatgagggt	ggagagcggg	tgctacagca	gcgctggacc	1140
	tccttcctca	aggcccagct	gctgtgctca	cggcccgacg	atggcttccc	cttcaacgtg	1200
	ctgcaggatg	tcttcacgct	gagccccagc	ccccaggact	ggcgtgacac	ccttttctat	1260
	ggggtcttca	cttcccagtg	gcacagggga	actacagaag	gctctgccgt	ctgtgtcttc	1320
	acaatgaagg	atgtgcagag	agtcttcagc	ggcctctaca	aggaggtgaa	ccgtgagaca	1380
	cagcagatgg	tacaccgtga	cccacccgtg	cccacacccc	ggcctggagc	gtgcatcacc	1440
	aacagtgccc	gggaaaggaa	gatcaactca	tccctgcagc	tcccagaccg	cgtgctgaac	1500
	ttcctcaagg	accacttcct	gatggacggg	caggtccgaa	gccgcatgct	gctgctgcag	1560
	ccccaggctc	gctaccagcg	cgtggctgta	caccgcgtcc	ctggcctgca	ccacacctac	1620
	gatgtcctct	tcctgggcac	tggtgacggc	cggctccaca	aggcagtgag	cgtgggcccc	1680
	cgggtgcaca	tcattgagga	gctgcagatc	ttctcatcgg	gacagcccgt	gcagaatctg	1740
	ctcctggaca	cccacagggg	gctgctgtat	gcggcctcac	actcgggcgt	agtccaggtg	1800
	cccatggcca	actgcagcct	gtacaggagc	tgtggggact	gcctcctcgc	ccgggacccc	1860
	tactgtgctt	ggagcggctc	cagctgcaag	cacgtcagcc	tctaccagcc	tcagctggcc	1920
	accaggccgt	ggatccagga	catcgaggga	gccagcgcca	aggacctttg	cagcgcgtct	1980
	tcggttgtgt	ccccgtcttt	tgtaccaaca	ggggagaagc	catgtgagca	agtccagttc	2040
	cagcccaaca	cagtgaacac	tttggcctgc	ccgctcctct	ccaacctggc	gacccgactc	2100
	tggctacgca	acggggcccc	cgtcaatgcc	tcggcctcct	gccacgtgct	acccactggg	2160
	gacctgctgc	tggtgggcac	ccaacagctg	ggggagttcc	agtgctggtc	actagaggag	2220
	ggcttccagc	agctggtagc	cagctactgc	ccagaggtgg	tggaggacgg	ggtggcagac	2280
	caaacagatg	agggtggcag	tgtacccgtc	attatcagca	catcgcgtgt	gagtgcacca	2340
	gctggtggca	aggccagctg	gggtgcagac	aggtcctact	ggaaggagtt	cctggtgatg	2400
	tgcacgctct	ttgtgctggc	cgtgctgctc	ccagttttat	tcttgctcta	ccggcaccgg	2460
	aacagcatga	aagtcttcct	gaagcagggg	gaatgtgcca	gcgtgcaccc	caagacctgc	2520
	cctgtggtgc	tgcccctga	gacccgccca	ctcaacggcc	tagggccccc	tagcaccccg	2580
	ctcgatcacc	gagggtacca	gtccctgtca	gacagccccc	cggggtcccg	agtcttcact	2640
	gagtcagaga	agaggccact	cagcatccaa	gacagcttcg	tggaggtatc	cccagtgtgc	2700
	ccccggcccc	gggtccgcct	tggctcggag	atccgtgact	ctgtggtgtg	agagctgact	2760
	tccagaggac	gctgccctgg	cttcaggggc	tgtgaatgct	cggagagggt	caactggacc	2820

tcccctccgc tctgctcttc gtggaacacg accgtggtgc ccggcccttg ggagccttgg 2940 ggccagctgg cctgctgctc tccagtcaag tagcgaagct cctaccaccc agacacccaa 3000 acagccgtgg ccccagaggt cctggccaaa tatgggggcc tgcctaggtt ggtggaacag tgctccttat gtaaactgag ccctttgttt aaaaaaacaat tccaaatgtg aaactagaat 3060 gagagggaag agatagcatg gcatgcagca cacacggctg ctccagttca tggcctccca 3120 3180 ggggtgctgg ggatgcatcc aaagtggttg tctgagacag agttggaaac cctcaccaac 3240 tggcctcttc accttccaca ttatcccgct gccaccggct gccctgtctc actgcagatt 3300 caggaccage ttgggetgeg tgcgttctge cttgccagte agecgaggat gtagttgttg 3360 ctgccgtcgt cccaccacct cagggaccag agggctaggt tggcactgcg gccctcacca ggtcctgggc tcggacccaa ctcctggacc tttccagcct gtatcaggct gtggccacac 3420 3480 gagaggacag cgcgagctca ggagagattt cgtgacaatg tacgcctttc cctcagaatt cagggaagag actgtcgcct gccttcctcc gttgttgcgt gagaacccgt gtgccccttc 3540 ccaccatatc caccctcgct ccatctttga actcaaacac gaggaactaa ctgcaccctg 3600 3660 gtcctctccc cagtccccag ttcaccctcc atccctcacc ttcctccact ctaagggata 3720 tcaacactgc ccagcacagg ggccctgaat ttatgtggtt tttatacatt ttttaataag 3766 atgcacttta tgtcattttt taataaagtc tgaagaatta ctgttt

<210> 10

<211> 837

<212> PRT

<213> Human

<400> 10

 Met
 Leu
 Arg
 Thr
 Ala
 Met
 Gly
 Leu
 Arg
 Ser
 Trp
 Leu
 Ala
 Ala
 Pro
 Trp

 Gly
 Ala
 Leu
 Pro
 Pro
 Arg
 Pro
 Pro
 Leu
 Inch
 Pro
 Pro
 Pro
 Pro
 Trp
 Ala
 Leu
 Leu
 Leu
 Leu
 Arg
 Inch
 Inch</td

Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala

			100					105					110		
Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys	Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln
		115					120					125			
Arg	Asp	Cys	Gln	Asn	Tyr	Ile	Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser
	130					135					140				
His	Leu	Phe	Thr	Cys	Gly	Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr
145					150					155					160
Ile	Asn	Met	Glu	Asn	Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val
				165					170					175	
Leu	Leu	Glu	Asp	Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys
			180					185					190		
Ser	Thr	Ala	Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser
		195					200					205			
Ser	Phe	Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg
	210					215					220				
Pro	Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe
225					230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	G1y	Asp
				245					250					255	
Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu	Phe	Glu
			260					265					270		
Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg			Lys	Gly
		275					280					285			
Asp	Glu	G1y	G1y	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp	Thr	Ser	Phe	Leu
	290					295					300		_		
Lys	Ala	G1n	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp	Gly	Phe	Pro	Phe	
305										315				_	320
Val	Leu	Gln	Asp			Thr	Leu	Ser			Pro	GIn	Asp		
				325					330		_			335	
Asp	Thr	Leu	Phe	Tyr	·Gly	Val	Phe			Gln	Trp	His			Ihr
			340					345					350		
Thr	Glu			Ala	l Val	Cys	Val		Thr	Met	Asr			GIn	Arg
		355					360				0.1	365		01	14 .
Val			Gly	/ Leu	ı Tyr		Glu	ı Val	Asr	n Arg			Glr	ı Gin	ı Met
	370			_	_	375					380		1		. 11
		s Arg	g Asp	Pro			Pro	Thr	r Pro			0 613	/ #18	ı Uys	
385	5				390)				395)				400

Thr	Asn	Ser	Ala	Arg	Glu	Arg	Lys	Ile	Asn	Ser	Ser	Leu	G1n	Leu	Pro	
				405					410					415		
Asp	Arg	Val	Leu	Asn	Phe	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln	
			420					425					430			
Val	Arg	Ser	Arg	Met	Leu	Leu	Leu	Gln	Pro	G1n	Ala	Arg	Tyr	G1n	Arg	
		435					440					445				
Val	Ala	Val	His	Arg	Val	Pro	Gly	Leu	His	His	Thr	Tyr	Asp	Val	Leu	
	450					455					460					
Phe	Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly	
465					470					475					480	
Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly	Gln	
				485					490					495		
Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu	Tyr	Ala	
			500					505					510			
Ala	Ser	His	Ser	Gly	Val	Val	Gln	Val	Pro	Met	Ala	Asn	Cys	Ser	Leu	
		515					520					525				
Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	
	530					535					540					
Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu	Tyr	Gln	Pro	Gln	Leu	
545					550					555					560	
Ala	Thr	Arg	Pro	Trp	Ile	Gln	Asp	Ile	Glu	Gly	Ala	Ser	Ala	Lys	Asp	
				565					570					575		
Leu	Cys	Ser	Ala	Ser	Ser	Val	Val			Ser	Phe	Val		Thr	Gly	
			580					585					590			
Glu	Lys	Pro	Cys	Glu	Gln	Val	Gln	Phe	Gln	Pro	Asn			Asn	Thr	
		595					600					605		_		
Leu	Ala	Cys	Pro	Leu	Leu			Leu	Ala	Thr			Trp	Leu	Arg	
	610					615			_	_	620			Б	TC1	
		Ala	Pro	Val			Ser	Ala	Ser			Val	Leu	Pro	Thr	
625					630				0.1	635		0.1	DI	01	640	
Gly	Asp	Leu	Leu			Gly	Thr	GIn			Gly	Glu	Pne		Cys	
				645				0.1	650			0	т.	655		
Trp	Ser	Leu			Gly	Phe	e Gln			ı Val	Ala	Ser			Pro	
			660					665		æ.		01	670		Com	
Glu	Val			ı Asp	Gly	v Val			Glr	Thr	Asp			Gly	Ser	
		675					680		•••	_		685		61	C1	
Val	Pro) Val	Ile	: Ile	Ser	Thi	Ser	٠Ar٤	y Val	Ser	. Als	1 Pro) Ala	Gly	Gly	

23/30

	690					695					700				
Lys	Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val
705					710					715					720
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	Leu
				725					730					735	
Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	Gly	Glu
			740					745					750		
Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	Pro	Pro	Glu
		755					760					765			
Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr	Pro	Leu	Asp	His
	770		•			775					780				
Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	Gly	Ser	Arg	Val	Phe
785					790					795					800
Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	Gln	Asp	Ser	Phe	Val	Glu
				805					810					815	
Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	Val	Arg	Leu	Gly	Ser	Glu	Ile
			820					825					830		
Arg	Asp	Ser	Val	Val											
		835													
											•				
<21	0> 1	1 .													
<21	1> 2	511													
<21	2> D	NA													
<21	3> H	uman													

<400> 11

60 atgctgcgca ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg cctcggccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc gccgcctccg 120 acctgggcgc tcagccccg gatcagcctg cctctgggct ctgaagagcg gccattcctc 180 240 agattcgaag ctgaacacat ctccaactac acagcccttc tgctgagcag ggatggcagg 300 accetgtacg tgggtgctcg agaggccctc tttgcactca gtagcaacct cagettcctg 360 ccaggcgggg agtaccagga gctgctttgg ggtgcagacg cagagaagaa acagcagtgc agcttcaagg gcaaggaccc acagcgcgac tgtcaaaact acatcaagat cctcctgccg 420 480 ctcagcggca gtcacctgtt cacctgtggc acagcagcct tcagccccat gtgtacctac 540 atcaacatgg agaacttcac cctggcaagg gacgagaagg ggaatgtcct cctggaagat 600 ggcaagggcc gttgtccctt cgacccgaat ttcaagtcca ctgccctggt ggttgatggc

gagctctaca	ctggaacagt	cagcagcttc	caagggaatg	acccggccat	ctcgcggagc	660
	gccccaccaa					720
	cctacattcc					780
	tcagcgagac					840
	gcatctgcaa					900
	tcaaggccca					960
gtgctgcagg	atgtcttcac	gctgagcccc	agcccccagg	actggcgtga	cacccttttc	1020
	tcacttccca					1080
ttcacaatga	atgatgtgca	gagagtcttc	agcggcctct	acaaggaggt	gaaccgtgag	1140
acacagcaga	tggtacaccg	tgacccaccc	gtgcccacac	cccggcctgg	agcgtgcatc	1200
	cccgggaaag					1260
aactttctca	aggaccactt	cctgatggac	gggcaggtcc	gaagccgcat	gctgctgctg	1320
cagccccagg	ctcgctacca	gcgcgtggct	gtacaccgcg	tccctggcct	gcaccacacc	1380
tacgatgtcc	tcttcctggg	cactggtgac	ggccggctcc	acaaggcagt	gagcgtgggc	1440
ccccgggtgc	acatcattga	ggagctgcag	atcttctcat	cgggacagcc	cgtgcagaat	1500
ctgctcctgg	acacccacag	ggggctgctg	tatgcggcct	cacactcggg	cgtagtccag	1560
gtgcccatgg	g ccaactgcag	cctgtaccgg	agctgtgggg	actgcctcct	cgcccgggac	1620
ccctactgtg	g cttggagcgg	ctccagctgc	aagcacgtca	gcctctacca	gcctcagctg	1680
gccaccaggo	cgtggatcca	ggacatcgag	ggagccagcg	ccaaggacct	ttgcagcgcg	1740
tcttcggttg	g tgtccccgtc	ttttgtacca	acaggggaga	agccatgtga	gcaagtccag	1800
ttccagccca	a acacagtgaa	cactttggcc	tgcccgctcc	tctccaacct	ggcgacccga	1860
ctctggctac	c gcaacggggc	ccccgtcaat	gcctcggcct	cctgccacgt	gctacccact	1920
ggggacctg	c tgctggtggg	cacccaacag	ctgggggagt	tccagtgct	g gtcactagag	1980
gagggcttc	c agcagctggt	agccagctac	tgcccagagg	g tggtggagga	a cggggtggca	2040
gaccaaaca	g atgagggtgg	cagtgtacco	gtcattatca	a gcacatcgcg	g tgtgagtgca	2100
ccagctggt	g gcaaggccag	g ctggggtgca	a gacaggtcc	t actggaagga	a gttcctggtg	2160
					t ctaccggcac	2220
cggaacagc	a tgaaagtctt	cctgaagcag	g ggggaatgt	g ccagcgtgc	a ccccaagacc	2280
					c ccctagcacc	2340
					c ccgagtcttc	2400
actgagtca	g agaagaggco	c actcagcato	caagacage	t tcgtggagg	t atccccagtg	2460
tgcccccgg	c cccgggtcc	g ccttggctc	g gagatccgt	g actctgtgg	t g	2511

⟨210⟩ 12

<211> 3766

<212> DNA

<213> Human

gctctgccca	agccgaggct	gcggggccgg	cgccggcggg	aggactgcgg	tgccccgcgg	60
aggggctgag	tttgccaggg	cccacttgac	cctgtttccc	acctcccgcc	ccccaggtcc	120
ggaggcgggg	gccccgggg	cgactcgggg	gcggaccgcg	gggcggagct	gccgcccgtg	180
agtccggccg	agccacctga	gcccgagccg	cgggacaccg	tcgctcctgc	tctccgaatg	240
ctgcgcaccg	cgatgggcct	gaggagctgg	ctcgccgccc	catggggcgc	gctgccgcct	300
cggccaccgc	tgctgctgct	cctgctgctg	ctgctcctgc	tgcagccgcc	gcctccgacc	360
tgggcgctca	gccccggat	cagcctgcct	ctgggctctg	aagagcggcc	attcctcaga	420
ttcgaagctg	aacacatctc	caactacaca	gcccttctgc	tgagcaggga	tggcaggacc	480
ctgtacgtgg	gtgctcgaga	ggccctcttt	gcactcagta	gcaacctcag	cttcctgcca	540
ggcggggagt	accaggagct	gctttggggt	gcagacgcag	agaagaaaca	gcagtgcagc	600
ttcaagggca	aggacccaca	gcgcgactgt	caaaactaca	tcaagatcct	cctgccgctc	660
agcggcagtc	acctgttcac	ctgtggcaca	gcagccttca	gccccatgtg	tacctacatc	720
aacatggaga	acttcaccct	ggcaagggac	gagaagggga	atgtcctcct	ggaagatggc	780
aagggccgtt	gtcccttcga	cccgaatttc	aagtccactg	ccctggtggt	tgatggcgag	840
ctctacactg	gaacagtcag	cagcttccaa	gggaatgacc	cggccatctc	gcggagccaa	900
agccttcgcc	ccaccaagac	cgagagctcc	ctcaactggc	tgcaagaccc	agcttttgtg	960
gcctcagcct	acattcctga	gagcctgggc	agcttgcaag	gcgatgatga	caagatctac	1020
tttttcttca	gcgagactgg	ccaggaattt	gagttctttg	agaacaccat	tgtgtcccgc	1080
attgcccgca	tctgcaaggg	cgatgagggt	ggagagcggg	tgctacagca	gcgctggac.c	1140
tccttcctca	aggcccagct	gctgtgctca	cggcccgacg	atggcttccc	cttcaacgtg	1200
ctgcaggatg	tcttcacgct	gagccccagc	ccccaggact	ggcgtgacac	ccttttctat	1260
ggggtcttca	cttcccagtg	gcacagggga	actacagaag	gctctgccgt	ctgtgtcttc	1320
acaatgaatg	atgtgcagag	agtcttcagc	ggcctctaca	aggaggtgaa	ccgtgagaca	1380
cagcagatgg	tacaccgtga	cccacccgtg	cccacacccc	ggcctggagc	gtgcatcacc	1440
aacagtgccc	gggaaaggaa	gatcaactca	tccctgcagc	tcccagaccg	cgtgctgaac	1500
tttctcaagg	g accacttcct	gatggacggg	caggtccgaa	gccgcatgct	gctgctgcag	1560
ccccaggcto	gctaccagcg	cgtggctgta	caccgcgtcc	ctggcctgca	ccacacctac	1620
gatgtcctct	tcctgggcac	tggtgacggc	cggctccaca	aggcagtgag	cgtgggcccc	1680
cgggtgcaca	ı tcattgagga	gctgcagato	ttctcatcgg	gacagcccgt	gcagaatctg	1740
ctcctggaca	a cccacagggg	gctgctgtat	geggeetead	actcgggcgt	agtccaggtg	1800
cccatggcca	a actgcagcct	gtaccggago	tgtggggact	gcctcctcgc	ccgggacccc	1860
tactgtgct1	ggagcggcto	cagctgcaag	g cacgtcagco	c tctaccagcc	tcagctggcc	1920
accaggccg1	t ggatccagga	catcgaggga	a gccagcgcca	a aggacctttg	cagcgcgtct	1980
tcggttgtg	t ccccgtcttt	tgtaccaaca	a ggggagaago	catgtgagca	agtccagttc	2040

cagcccaaca	cagtgaacac	tttggcctgc	ccgctcctct	ccaacctggc	gacccgactc	2100
tggctacgca	acggggcccc	cgtcaatgcc	tcggcctcct	gccacgtgct	acccactggg	2160
gacctgctgc	tggtgggcac	ccaacagctg	ggggagttcc	agtgctggtc	actagaggag	2220
ggcttccagc	agctggtagc	cagctactgc	ccagaggtgg	tggaggacgg	ggtggcagac	2280
caaacagatg	agggtggcag	tgtacccgtc	attatcagca	catcgcgtgt	gagtgcacca	2340
gctggtggca	aggccagctg	gggtgcagac	aggtcctact	ggaaggagtt	cctggtgatg	2400
			ccagttttat			2460
			gaatgtgcca			2520
			ctcaacggcc			2580
			gacagccccc			2640
			gacagcttcg			2700
			atccgtgact			2760
tccagaggac	gctgccctgg	cttcaggggc	tgtgaatgct	cggagagggt	caactggacc	2820
			accgtggtgc			2880
ggccagctgg	cctgctgctc	tccagtcaag	tagcgaagct	cctaccaccc	agacacccaa	2940
acagccgtgg	ccccagaggt	cctggccaaa	tatgggggcc	tgcctaggtt	ggtggaacag	3000
tgctccttat	gtaaactgag	ccctttgttt	aaaaaacaat	tccaaatgtg	aaactagaat	3060
gagagggaag	agatagcatg	gcatgcagca	cacacggctg	ctccagttca	tggcctccca	3120
ggggtgctgg	ggatgcatcc	aaagtggttg	tctgagacag	agttggaaac	cctcaccaac	3180
tggcctcttc	accttccaca	ttatcccgct	gccaccggct	gccctgtctc	actgcagatt	3240
caggaccagc	ttgggctgcg	tgcgttctgc	cttgccagtc	agccgaggat	gtagttgttg	3300
ctgccgtcgt	cccaccacct	cagggaccag	agggctaggt	tggcactgcg	gccctcacca	3360
ggtcctgggc	tcggacccaa	ctcctggacc	tttccagcct	gtatcaggct	gtggccacac	3420
gagaggacag	cgcgagctca	ggagagattt	cgtgacaatg	tacgcctttc	cctcagaatt	3480
cagggaagag	actgtcgcct	gccttcctcc	gttgttgcgt	gagaacccgt	gtgccccttc	3540
ccaccatatc	caccctcgct	ccatctttga	actcaaacac	gaggaactaa	ctgcaccctg	3600
gtcctctccc	cagtccccag	ttcaccctcc	atccctcacc	ttcctccact	ctaagggata	3660
tcaacactgc	ccagcacagg	ggccctgaat	ttatgtggtt	titatacatt	ttttaataag	3720
atgcacttta	tgtcattttt	taataaagto	tgaagaatta	ctgttt		3766

⟨210⟩ 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

 $\langle 223 \rangle$ Oligonucleotide

N4007 13	
cagtgccaac ctagccctct	20
<210> 14	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Oligonucleotide	
<400> 14	
tctcccgatc caaccgtgac	20
<210> 15	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Oligonucleotide	
<400> 15	
(4007-13	
caacaactac atcctcggct	20
<210> 16	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	

 $\langle 223 \rangle$ Oligonucleotide

<400> 16

tcggctccta catcaacaac	20
<210> 17	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
4400 47	
<400> 17	
cctcgcccgg gacccctact gtgc	24
coregeous saccouract gige	27
<210> 18	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 18	
cttggcgctg gctccctcga tgtcctg	27
Citiggogotic gottocotic testocity	
<210> 19	
<211> 28	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	

aattgaattc atgctgcgca ccgcgatg	28
<210≻ 20	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 20	
aagctctaga caccacagag tcacggatct	30
<210> 21	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<pre><223> Primer</pre>	
<400> 21	
	,
aagctctaga tcacaccaca gagtcacgga	30
<210> 22	
<211> 12	
<212> PRT	
<213> Human	
<400> 22	
Acr Sor Ala Ara Clu Ara luc Ila Acr Sor Sor Cvs	

30/30 <210> 23 <211> 15 <212> PRT <213> Human <400> 23 Ser Val Val Ser Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys 5 10 15 <210> 24 <211> 15 <212> PRT <213> Human <400> 24 Pro Leu Asp His Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Cys 5 10 15 <210> 25 <211> 14 <212> PRT <213> Human

<400> 25

Ser Arg Val Phe Thr Glu Ser Glu Lys Arg Pro Leu Ser Cys